

Table S1: LIGER parameter settings of analyses featured in main figure panels. Related to Figure STAR Methods.

<u>Analysis</u>	<u>Figure</u>	<u>k</u>	<u>lambda</u>	<u>knn_k</u>	<u>resolution</u>	<u>k2 (for mem efficiency)</u>	<u>min_cells</u>	<u>Comparison</u>
PBMC	2	22	5	20	0.4	500	2	Different scRNA-seq technologies
Mouse/human pancreas	2	35	15	20	0.8	440	2	Human vs. mouse
Interneurons/ oligodendr.	2	40	5	20	4	480	10	Divergent cell types
BNST neurons	3	60	1	NA	NA	NA	NA	Male vs. female
BNST-CGE cortex	3	15	5	20	0.25	500	10	Cross tissue; nuclei vs. cells
BNST-striatal SPN	3	25	5	20	2.5	500	10	Cross tissue; nuclei vs. cells
Substantia nigra, human nuclei	4	30	20	15	0.3	500	2	Across 7 postmortem human subjects
scRNA/STARmap	5	30	5	20	0.1	500	2	STARmap vs. scRNA-seq
scRNA/methyl.	6	25	5	20	0.1	500	2	scRNA-seq vs. methylation